SEQUENCE LISTING

<110> Jay Short
Eric Mathur
William Michael Lafferty
Nelson Barton
Kevin Chow

<120> Method of Making a Protein Polymer and Uses of the Polymer

<130> 564462010900

<140> 09/997,807
<141> 2001-11-30

<150> 60/250,426
<151> 2000-11-30

<160> 37

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 624
<212> DNA
<213> Pyrodictium abyssi

<400> 1
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ctagcaggct tcgccaccac ccagagcccc ctcaacagct tctacgccac cggtacagca 120
caggcagtaa gcgagccaat agacgtagaa agccacctcg gcagcataac ccccgcagcc 180
ggcgcacagg gcagtgacga cataggttac gcaatagtgt ggataaagga ccaggtcaat 240
gatgtaaagc tgaaggtgac cctgcgtaac gctgagcagc taaagcccta cttcaagtac 300
ctacagatac agataacaag cggctatgag acgaacagca cagctctagg caacttcagc 360
gagaccaagg ctgtgataag cctcgacaac cccagcgccg tgatagtact agacaaggag 420
gatatagcag tgctctatcc ggacaagacc ggttacacaa acacttcgat atgggtaccc 480
ggtgaacctg acaagataat tgtctacaac gagacaaagc cagtagctat actgaacttc 540
aaggccttct acgaggctaa ggagggtatg ctattcgaca gcctgccagt gatattcaac 600
ttccaggtgc tacaagtagg ctaa 624

<210> 2
<211> 207
<212> PRT
<213> Pyrodictium abyssi

<400> 2
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Ala Leu Ala Leu Leu Ala Gly Phe Ala Thr Thr Gln Ser Pro Leu Asn
20 25 30
Ser Phe Tyr Ala Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp
35 40 45
Val Glu Ser His Leu Gly Ser Ile Thr Pro Ala Ala Gly Ala Gln Gly
50 55 60
Ser Asp Asp Ile Gly Tyr Ala Ile Val Trp Ile Lys Asp Gln Val Asn
65 70 75 80
Asp Val Lys Leu Lys Val Thr Leu Arg Asn Ala Glu Gln Leu Lys Pro
85 90 95

Tyr Phe Lys Tyr Leu Gln Ile Gln Ile Thr Ser Gly Tyr Glu Thr Asn
100 105 110
Ser Thr Ala Leu Gly Asn Phe Ser Glu Thr Lys Ala Val Ile Ser Leu
115 120 125
Asp Asn Pro Ser Ala Val Ile Val Leu Asp Lys Glu Asp Ile Ala Val
130 135 140
Leu Tyr Pro Asp Lys Thr Gly Tyr Thr Asn Thr Ser Ile Trp Val Pro
145 150 155 160
Gly Glu Pro Asp Lys Ile Ile Val Tyr Asn Glu Thr Lys Pro Val Ala
165 170 175
Ile Leu Asn Phe Lys Ala Phe Tyr Glu Ala Lys Glu Gly Met Leu Phe
180 185 190
Asp Ser Leu Pro Val Ile Phe Asn Phe Gln Val Leu Gln Val Gly
195 200 205

<210> 3
<211> 513
<212> DNA
<213> Pyrodictium abyssi

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gccgcaacaa gcgagccaat agacgtagag agccacctca gcagcatagc ccctgctgct 180
ggcgcacagg gcagccagga cataggctac ttcaacgtga ccgccaagga tcaagtgaac 240
gtgacaaaga taaaggtgac cctggctaac gctgagcagc taaagcccta cttcaagtac 300
ctacagatag tgctaaagag cgaggtagct gacgagatca aggccgtaat aagcatagac 360
aagcctagcg ccgtcataat actagacagc caggacttcg acagcaacaa cagagcaaag 420
ataagcgcca ctgcctacta cgaggctaag gagggcatgc tattcgacag cctaccgcta 480
atattcaaca tacaggtgct aagcgtcagc taa 513

<210> 4
<211> 170
<212> PRT
<213> Pyrodictium abyssi

<400> 4
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20 25 30
Ser Phe Tyr Ala Thr Gly Thr Ala Ala Ala Thr Ser Glu Pro Ile Asp
35 40 45
Val Glu Ser His Leu Ser Ser Ile Ala Pro Ala Ala Gly Ala Gln Gly
50 55 60
Ser Gln Asp Ile Gly Tyr Phe Asn Val Thr Ala Lys Asp Gln Val Asn
65 70 75 80
Val Thr Lys Ile Lys Val Thr Leu Ala Asn Ala Glu Gln Leu Lys Pro
85 90 95
Tyr Phe Lys Tyr Leu Gln Ile Val Leu Lys Ser Glu Val Ala Asp Glu
100 105 110
Ile Lys Ala Val Ile Ser Ile Asp Lys Pro Ser Ala Val Ile Ile Leu
115 120 125
Asp Ser Gln Asp Phe Asp Ser Asn Asn Arg Ala Lys Ile Ser Ala Thr
130 135 140
Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu Phe Asp Ser Leu Pro Leu
145 150 155 160
Ile Phe Asn Ile Gln Val Leu Ser Val Ser
165 170

<210> 5
<211> 537
<212> DNA
<213> Pyrodictium abyssi

<400> 5
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ctagcaggct tcgccacgac ccagagcccg ctaagcagct tctacgccac cggcacagca 120
caagcagtaa gcgagccaat agacgtagag agccacctag acaacaccat agcccctgct 180
gccggtgcac agggctacaa ggacatgggc tacattaaga taactaacca gtcaaaagtt 240
aatgtaataa agctgaaggt gactctcgct aacgccgagc agctaaagcc ctacttcgac 300
tacctacagc tagtactcac aagcaacgcc actggcaccg acatggttaa ggctgtgcta 360
agcctcgaga agcctagcgc agtcataata ctagacaacg atgactacga tagcactaac 420
aagatacagc taaaggtaga agcctactat gaggctaagg agggcatgct attcgacagc 480
ctaccagtaa tactgaactt ccaggtactg agcgccgctt gcagtccctt gtggtga 537

<210> 6
<211> 178
<212> PRT
<213> Pyrodictium abyssi

<400> 6
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Ala Leu Ala Leu Leu Ala Gly Phe Ala Thr Thr Gln Ser Pro Leu Ser
20 25 30
Ser Phe Tyr Ala Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp
35 40 45
Val Glu Ser His Leu Asp Asn Thr Ile Ala Pro Ala Ala Gly Ala Gln
50 55 60
Gly Tyr Lys Asp Met Gly Tyr Ile Lys Ile Thr Asn Gln Ser Lys Val
65 70 75 80
Asn Val Ile Lys Leu Lys Val Thr Leu Ala Asn Ala Glu Gln Leu Lys
85 90 95
Pro Tyr Phe Asp Tyr Leu Gln Leu Val Leu Thr Ser Asn Ala Thr Gly
100 105 110
Thr Asp Met Val Lys Ala Val Leu Ser Leu Glu Lys Pro Ser Ala Val
115 120 125
Ile Ile Leu Asp Asn Asp Asp Tyr Asp Ser Thr Asn Lys Ile Gln Leu
130 135 140
Lys Val Glu Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu Phe Asp Ser
145 150 155 160
Leu Pro Val Ile Leu Asn Phe Gln Val Leu Ser Ala Ala Cys Ser Pro
165 170 175
Leu Trp

<210> 7
<211> 395
<212> DNA
<213> Pyrodictium abyssi

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ctcggtacgc taaatactgc cgctggtgca cagggtaagc agacgctagg agacataaca 120
atatatgcgc acaatgacgt gaacataaca aagctaaagg tcacgcttgc taacgctgca 180
cagctaagac catacttcaa gtacctgata ataaagctag taagcctgga cagcaacggc 240
aacgagtccg aggaaaaggg catgataact ctatggaagc cttacgccgt gataatacta 300

gaccatgaag atttcaacaa cgacatcgac aatgacggca acaatgacgc caagataagg 360
gttgtagcct actatgaggc taaggagggt atgct 395

<210> 8
<211> 131
<212> PRT
<213> Pyrodictium abyssi

<400> 8
Ser Phe Tyr Ala Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp
1 5 10 15
Val Val Ser Ser Leu Gly Thr Leu Asn Thr Ala Ala Gly Ala Gln Gly
20 25 30
Lys Gln Thr Leu Gly Asp Ile Thr Ile Tyr Ala His Asn Asp Val Asn
35 40 45
Ile Thr Lys Leu Lys Val Thr Leu Ala Asn Ala Ala Gln Leu Arg Pro
50 55 60
Tyr Phe Lys Tyr Leu Ile Ile Lys Leu Val Ser Leu Asp Ser Asn Gly
65 70 75 80
Asn Glu Ser Glu Glu Lys Gly Met Ile Thr Leu Trp Lys Pro Tyr Ala
85 90 95
Val Ile Ile Leu Asp His Glu Asp Phe Asn Asn Asp Ile Asp Asn Asp
100 105 110
Gly Asn Asn Asp Ala Lys Ile Arg Val Val Ala Tyr Tyr Glu Ala Lys
115 120 125
Glu Gly Met
130

<210> 9
<211> 372
<212> DNA
<213> Pyrodictium abyssi

<400> 9
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acaatagaga acaagactga cgtgaacgtt gtgaagctga agataaccct cgccaacgct 180
gagcagctaa agccctactt cgactaccta cagatagtgc taaagagcgt tgacagcaac 240
gagatcaagg ctgtgctaag cctcgagaag cccagcgcag tcataatact ggacaacgag 300
gacttccagg gcggcgacaa ccagtgccag atagacgcca ccgcctacta cgaggctaag 360
gagggtatgc ta 372

<210> 10
<211> 124
<212> PRT
<213> Pyrodictium abyssi

<400> 10
Ser Phe Tyr Ala Thr Gly Thr Ala Glu Ala Thr Ser Glu Pro Ile Asp
1 5 10 15
Val Val Ser Asn Leu Asn Thr Ala Ile Ala Pro Ala Ala Gly Ala Gln
20 25 30
Gly Ser Val Gly Ile Gly Ser Ile Thr Ile Glu Asn Lys Thr Asp Val
35 40 45
Asn Val Val Lys Leu Lys Ile Thr Leu Ala Asn Ala Glu Gln Leu Lys
50 55 60
Pro Tyr Phe Asp Tyr Leu Gln Ile Val Leu Lys Ser Val Asp Ser Asn
65 70 75 80
Glu Ile Lys Ala Val Leu Ser Leu Glu Lys Pro Ser Ala Val Ile Ile

85 90 95
Leu Asp Asn Glu Asp Phe Gln Gly Gly Asp Asn Gln Cys Gln Ile Asp
100 105 110
Ala Thr Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu
115 120

<210> 11
<211> 448
<212> DNA
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 11
tgagacccta gctgcggatt gcctcggctg ccgcctcgcc ctctagcagg cttcgccaca 60
cccagagccc ctacagcttc tacgccaccg gcacagcaca ggcagtaagc gagccaatag 120
acgtagaaag ccacctcaca catagcccct gctgccggcg cacagggcag caggacatag 180
gctacataaa ataacaagat agtgaacgta taaagctgaa ggtgaccctg ctaacgctga 240
gcagctaaag ccctacttca agtacctaca gatagtgcta aaagcgacag caggcacacg 300
agaaggcgtg ataagcctcg agaagcctag cgccgtcata atactagaca acgaggactt 360
cgaagcacaa cagaaagaga agcaatagcc tactacgagg ctaaggaggg tatgctattc 420
gacagcctcc tatataactc aggtctgt 448

<210> 12
<211> 140
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<400> 12
Val Lys Thr Leu Ala Leu Ala Gly Ile Ile Ala Ser Ala Ala Leu Ala
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20 25 30
Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp Val Glu Ser His
35 40 45
Leu Ser Ile Ala Pro Ala Ala Gly Ala Gln Gly Ser Asp Ile Gly Tyr
50 55 60
Ile Ile Lys Val Asn Val Val Lys Leu Lys Val Thr Leu Ala Asn Ala
65 70 75 80
Glu Gln Leu Lys Pro Tyr Phe Lys Tyr Leu Gln Ile Val Leu Ser Ser
85 90 95
Glu Ile Lys Ala Val Ile Ser Leu Asp Lys Pro Ser Ala Val Ile Ile
100 105 110
Leu Asp Glu Asp Phe Ala Ile Ala Tyr Tyr Glu Ala Lys Glu Gly Met
115 120 125
Leu Phe Asp Ser Leu Pro Val Ile Asn Gln Val Leu
130 135 140

<210> 13
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker peptide

<400> 13
Gly Gly Gly Gly Ser
 1   5

<210> 14
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide sequence of a restriction site

<400> 14
cgcgctggac 10

<210> 15
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
aagggaggag 10

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
ctagaagaga ggagaaaacc atg 23

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
gatcaaaggc gcgcctgcag g 21

<210> 18
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 18
ctagaaggga ggagaaaacc atg 23

<210> 19
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
gatcaaaggc gcgcctgcag g 21

<210> 20
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide sequence of a cleavage site

<221> unsure
<222> (0)...(0)
<223> N = A, G, C or T

<400> 20
gagtcnnnnn 10

<210> 21
<211> 22
<212> DNA
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<220>
<223> Oligonucleotide

<400> 21
gccagggttt tcccagtcac ga 22

<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 22
agcggataac aatttcacac agg 23

<210> 23
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 23
attaaccctc actaaag 17

<210> 24
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 24
taatacgact cactataggg g 21

<210> 25
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 25
ctagttattg ctcagcgg 18

<210> 26
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 26
cagagccccg ctcaa 15

<210> 27
<211> 20
<212> DNA
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<220>
<223> Oligonucleotide

<400> 27
gcagctaaag ccctacttca 20

<210> 28
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 28
cagcttctac gccaccgg 18

<210> 29
<211> 21
<212> DNA

<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 29
tgtgaagtac acaaccctag c 21

<210> 30
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 30
gcgccggctg cggggg 16

<210> 31
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

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ctgtgctgta ccggtggcg 19

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 32
agcataccct ccttagcctc 20

<210> 33
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 33
tagcaggcca tatgaccacc cagagccccc 30

<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 34
ctagcaggcc atatgacgac ccagagcc 28

<210> 35
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 35
ggaggactgg cggccgctgt tagcctac 28

<210> 36
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 36
agtagctagc ggccgcttta gctgacgc 28

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 37
ggccgtggcg gccgctgctt cacc 24